



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/789,818

DATE: 08/06/2004

TIME: 14:14:07

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Output Set: N:\CRF4\08062004\J789818.raw

3 <110> APPLICANT: IBRAHIM, PRABHA
 4 KRUPKA, HEIKE
 5 KUMAR, ABHINAV
 6 MILBURN, MICHAEL V.
 7 SUZUKI, YOSHIHISA
 9 <120> TITLE OF INVENTION: PYK2 CRYSTAL STRUCTURE AND USES
 11 <130> FILE REFERENCE: 039363/1202
 13 <140> CURRENT APPLICATION NUMBER: 10/789,818
 14 <141> CURRENT FILING DATE: 2004-02-27
 16 <150> PRIOR APPLICATION NUMBER: 60/451,101
 17 <151> PRIOR FILING DATE: 2003-02-28
 19 <160> NUMBER OF SEQ ID NOS: 25
 21 <170> SOFTWARE: PatentIn Ver. 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 272
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Homo sapiens
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 30 1 5 10 15
 32 Phe Gly Glu Val Tyr Glu Gly Val Tyr Thr Asn His Lys Gly Glu Lys
 33 20 25 30
 35 Ile Asn Val Ala Val Lys Thr Cys Lys Lys Asp Cys Thr Leu Asp Asn
 36 35 40 45
 38 Lys Glu Lys Phe Met Ser Glu Ala Val Ile Met Lys Asn Leu Asp His
 39 50 55 60
 41 Pro His Ile Val Lys Leu Ile Gly Ile Ile Glu Glu Glu Pro Thr Trp
 42 65 70 75 80
 44 Ile Ile Met Glu Leu Tyr Pro Tyr Gly Glu Leu Gly His Tyr Leu Glu
 45 85 90 95
 47 Arg Asn Lys Asn Ser Leu Lys Val Leu Thr Leu Val Leu Tyr Ser Leu
 48 100 105 110
 50 Gln Ile Cys Lys Ala Met Ala Tyr Leu Glu Ser Ile Asn Cys Val His
 51 115 120 125
 53 Arg Asp Ile Ala Val Arg Asn Ile Leu Val Ala Ser Pro Glu Cys Val
 54 130 135 140
 56 Lys Leu Gly Asp Phe Gly Leu Ser Arg Tyr Ile Glu Asp Glu Asp Tyr
 57 145 150 155 160
 59 Tyr Lys Ala Ser Val Thr Arg Leu Pro Ile Lys Trp Met Ser Pro Glu
 60 165 170 175
 62 Ser Ile Asn Phe Arg Arg Phe Thr Thr Ala Ser Asp Val Trp Met Phe
 63 180 185 190
 65 Ala Val Cys Met Trp Glu Ile Leu Ser Phe Gly Lys Gln Pro Phe Phe



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66      195      200      205
68 Trp Leu Glu Asn Lys Asp Val Ile Gly Val Leu Glu Lys Gly Asp Arg
69      210      215      220
71 Leu Pro Lys Pro Asp Leu Cys Pro Pro Val Leu Tyr Thr Leu Met Thr
72 225      230      235      240
74 Arg Cys Trp Asp Tyr Asp Pro Ser Asp Arg Pro Arg Phe Thr Glu Leu
75      245      250      255
77 Val Cys Ser Leu Ser Asp Val Tyr Gln Met Glu Lys Asp Ile Ala Met
78      260      265      270
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84 <212> TYPE: PRT
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87 <220> FEATURE:
88 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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93  1      5      10      15
95 Arg Gly Ser His Met Ile Ala Arg Glu Asp Val Val Leu Asn Arg Ile
96      20      25      30
98 Leu Gly Glu Gly Phe Phe Gly Glu Val Tyr Glu Gly Val Tyr Thr Asn
99      35      40      45
101 His Lys Gly Glu Lys Ile Asn Val Ala Val Lys Thr Cys Lys Lys Asp
102      50      55      60
104 Cys Thr Leu Asp Asn Lys Glu Lys Phe Met Ser Glu Ala Val Ile Met
105 65      70      75      80
107 Lys Asn Leu Asp His Pro His Ile Val Lys Leu Ile Gly Ile Ile Glu
108      85      90      95
110 Glu Glu Pro Thr Trp Ile Ile Met Glu Leu Tyr Pro Tyr Gly Glu Leu
111      100      105      110
113 Gly His Tyr Leu Glu Arg Asn Lys Asn Ser Leu Lys Val Leu Thr Leu
114      115      120      125
116 Val Leu Tyr Ser Leu Gln Ile Cys Lys Ala Met Ala Tyr Leu Glu Ser
117      130      135      140
119 Ile Asn Cys Val His Arg Asp Ile Ala Val Arg Asn Ile Leu Val Ala
120 145      150      155      160
122 Ser Pro Glu Cys Val Lys Leu Gly Asp Phe Gly Leu Ser Arg Tyr Ile
123      165      170      175
125 Glu Asp Glu Asp Tyr Tyr Lys Ala Ser Val Thr Arg Leu Pro Ile Lys
126      180      185      190
128 Trp Met Ser Pro Glu Ser Ile Asn Phe Arg Arg Phe Thr Thr Ala Ser
129      195      200      205
131 Asp Val Trp Met Phe Ala Val Cys Met Trp Glu Ile Leu Ser Phe Gly
132      210      215      220
134 Lys Gln Pro Phe Phe Trp Leu Glu Asn Lys Asp Val Ile Gly Val Leu
135 225      230      235      240
137 Glu Lys Gly Asp Arg Leu Pro Lys Pro Asp Leu Cys Pro Pro Val Leu
138      245      250      255

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140 Tyr Thr Leu Met Thr Arg Cys Trp Asp Tyr Asp Pro Ser Asp Arg Pro
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143 Arg Phe Thr Glu Leu Val Cys Ser Leu Ser Asp Val Tyr Gln Met Glu
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147           290
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157 tatgaagggtg tctacacaaa tcacaaaggg gagaaatca atgtagctgt caagacctgc 120
158 aagaaagact gcactctgga caacaaggag aagttcatga gcgaggcagt gatcatgaag 180
159 aacctcgacc acccgcacat cgtgaagctg atcggcacat ttgaagagga gcccacctgg 240
160 atcatcatgg aattgtatcc ctatggggag ctggggccact acctggagcg gaacaagaac 300
161 tccctgaagg tgctcaccct cgtgctgtac tctactgcaga tatgcaaagc catggcctac 360
162 ctggagagca tcaactgcgt gcacaggac attgctgtcc ggaacatcct ggtggcctcc 420
163 cctgagtgtg tgaagctggg ggacttttgg ctttcccggt acattgagga cgaggactat 480
164 tacaaagcct ctgtgactcg tctccccatc aaatggatgt ccccagagtc cattaacttc 540
165 cgacgcttca cgacagccag tgacgtctgg atgttcgccg tgtgcatgtg ggagatcctg 600
166 agctttggga agcagccctt cttctggctg gagaacaagg atgtcatcgg ggtgctggag 660
167 aaaggagacc ggctgcccac gctgatctc tgtccaccgg tcctttatac cctcatgacc 720
168 cgctgctggg actacgaccc cagtgaccgg ccccgcttca ccgagctggg gtgcagcctc 780
169 agtgacgttt atcagatgga gaaggacatt gccatg 816
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173 <211> LENGTH: 1050
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
179      pET15S nucleotide sequence
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182 tctagaaata attttgttta actttaagaa ggagatatac catgggcagc agccatcatc 60
183 atcatcatca cagcagcggc ctggtgccgc gcggcagcca tatgattgcc cgtgaagatg 120
184 tggtcctgaa tcgtattctt ggggaaggct tttttgggga ggtctatgaa ggtgtctaca 180
185 caaatcacia aggggagaaa atcaatgtag ctgtcaagac ctgcaagaaa gactgcactc 240
186 tggacaacaa ggagaagttc atgagcgagg cagtgatcat gaagaacctc gaccacccgc 300
187 acatcgtgaa gctgatcggc atcattgaag aggagccac ctggatcatc atggaattgt 360
188 atccctatgg ggagctgggc cactacctgg agcggaaaca gaactccctg aagggtgctc 420
189 ccctcgtgct gtactcactg cagatatgca aagccatggc ctacctggag agcatcaact 480
190 gcgtgcacag ggacattgct gtccggaaca tcctggtggc ctcccctgag tgtgtgaagc 540
191 tgggggactt tgggtcttcc cggtagattg aggacgagga ctattacaaa gcctctgtga 600
192 ctcgctctcc catcaaatgg atgtcccag agtccattaa cttccgacgc ttcacgacag 660
193 ccagtgaagt ctggatgttc gccgtgtgca tgtgggagat cctgagcttt gggaagcagc 720
194 ccttcttctg gctggagaac aaggatgtca tcggggtgct ggagaaagga gaccggctgc 780
195 ccaagcctga tctctgtcca ccggtccttt ataccctcat gaccgctgc tgggactacg 840
196 accccagtga ccggccccgc ttcaccgagc tgggtgtgcag cctcagtgcg gtttatcaga 900
197 tggagaagga cattgccatg taggtcgact agagcctgca gtctcgacca tcatcatcat 960

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198 catcattaat aaaagggcga attccagcac actggcgcc gttactagt gatccggctg 1020
199 ctaacaaagc ccgaaaggaa gctgagttgg 1050
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203 <211> LENGTH: 33
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
207 <220> FEATURE:
208 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
210 <400> SEQUENCE: 5
211 tccacagcat atgattgccc gtgaagatgt ggt 33
214 <210> SEQ ID NO: 6
215 <211> LENGTH: 34
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
222 <400> SEQUENCE: 6
223 ctctcgtcga cctacatggc aatgtccttc tcca 34
226 <210> SEQ ID NO: 7
227 <211> LENGTH: 391
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <221> NAME/KEY: CDS
233 <222> LOCATION: (108)..(170)
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
237 pET15S multi-cloning site nucleotide sequence
239 <400> SEQUENCE: 7
240 agatctcgat cccgcgaaat taatacgact cactataggg gaattgtgag cggataacaa 60
242 ttcccctcta gaaataattt tgtttaactt taagaaggag atatacc atg ggc agc 116
243 Met Gly Ser
244 1
246 agc cat cat cat cat cat cac agc agc ggc ctg gtg ccg cgc ggc agc 164
247 Ser His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
248 5 10 15
250 cat atg ggatccggaa ttcaaaggcc tacgtcgact agagcctgca gtctcgacca 220
251 His Met
252 20
254 tcatcatcat catcattaat aaaagggcga attccagcac actggcgcc gttactagt 280
256 gatccggctg ctaacaaagc ccgaaaggaa gctgagttgg ctgctgccac cgctgagcaa 340
258 taactagcat aaccccttgg ggcctctaaa cgggtcttga ggggtttttt g 391
261 <210> SEQ ID NO: 8
262 <211> LENGTH: 21
263 <212> TYPE: PRT
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
268 pET15S multi-cloning site peptide sequence

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275           20
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284 <213> ORGANISM: Unknown Organism
286 <220> FEATURE:
287 <223> OTHER INFORMATION: Description of Unknown Organism: FAK tyrosine kinase
288     sequence
290 <400> SEQUENCE: 9
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292   1           5           10           15
294 Gln Phe Gly Asp Val His Gln Gly Ile Tyr Met Ser Pro Glu Asn Pro
295           20           25           30
297 Ala Leu Ala Val Ala Ile Lys Thr Cys Lys Asn Cys Thr Ser Asp Ser
298           35           40           45
300 Val Arg Glu Lys Phe Leu Gln Glu Ala Cys His Tyr Thr Ser Leu His
301           50           55           60
303 Trp Asn Trp Cys Arg Tyr Ile Ser Asp Pro Asn Val Asp Ala Cys Pro
304           65           70           75           80
306 Asp Pro Arg Asn Ala Glu Leu Thr Met Arg Gln Phe Asp His Pro His
307           85           90           95
309 Ile Val Lys Leu Ile Gly Val Ile Thr Glu Asn Pro Val Trp Ile Ile
310           100          105          110
312 Met Glu Leu Cys Thr Leu Gly Glu Leu Arg Ser Phe Leu Gln Val Arg
313           115          120          125
315 Lys Tyr Ser Leu Asp Leu Ala Ser Leu Ile Leu Tyr Ala Tyr Gln Leu
316           130          135          140
318 Ser Thr Ala Leu Ala Tyr Leu Glu Ser Lys Arg Phe Val His Arg Asp
319           145          150          155          160
321 Ile Ala Ala Arg Asn Val Leu Val Ser Ser Asn Asp Cys Val Lys Leu
322           165          170          175
324 Gly Asp Phe Gly Leu Ser Arg Tyr Met Glu Asp Ser Thr Tyr Tyr Lys
325           180          185          190
327 Ala Ser Lys Gly Lys Leu Pro Ile Lys Trp Met Ala Pro Glu Ser Ile
328           195          200          205
330 Asn Phe Arg Arg Phe Thr Ser Ala Ser Asp Val Trp Met Phe Gly Val
331           210          215          220
333 Cys Met Trp Glu Ile Leu Met His Gly Val Lys Pro Phe Gln Gly Val
334           225          230          235          240
336 Lys Asn Asn Asp Val Ile Gly Arg Ile Glu Asn Gly Glu Arg Leu Pro
337           245          250          255
339 Met Pro Pro Asn Cys Pro Pro Thr Leu Tyr Ser Leu Met Thr Lys Cys
340           260          265          270
342 Trp Ala Tyr Asp Pro Ser Arg Arg Pro Arg Phe Thr Glu Leu Lys Ala
343           275          280          285

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VERIFICATION SUMMARY

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